

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: LI, Yi and RUBEN, Steven M.
- (ii) TITLE OF INVENTION: HUMAN AMINE RECEPTOR POLYPEPTIDES
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN AND FOX, P.L.L.C.
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  - (C) CITY: WASHINGTON
  - (D) STATE: DC
  - (E) COUNTRY: UNITED STATES OF AMERICA
  - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 09/314,006
  - (B) FILING DATE: 19-MAY-1999
  - (C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: US 08/467,559
  - (B) FILING DATE: 06-JUN-1995
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: STEFFE, ERIC K
  - (B) REGISTRATION NUMBER: 36,688
  - (C) REFERENCE/DOCKET NUMBER: 1488.0840001/EKS/HCC
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (202) 371-2600
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1380 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
- (A) NAME/KEY: CDS

093145 54288660

(B) LOCATION: 252..1262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTAGAGCTAG CAGGAGTAAC TCTCATGGAA CCTTGAAAC CATTCTTCAA TTGAATTTC	60
GGGCACATTT GAATCAGTAC CCAGGGGCAC TGTACTATGC TCCCAGCTGG ACCTTAGTTT	120
CCTCCTCCTC GTTTCACCCT GTGAGTAATT AACAGACAAA ATTTTTTTTTT TTTTTTTTTT	180
TTTTTTTTTT TTTTGGCCCT CCAGTGGAGA AGGTGGCCAG TTCTCAGACA GAGGAAGAGT	240
AGAAATCATA A ATG AGA GCT GTC TTC ATC CAA GGT GCT GAA GAG CAC CCT	290
Met Arg Ala Val Phe Ile Gln Gly Ala Glu Glu His Pro	
1 5 10	
GCG GCA TTC TGC TAC CAG GTG AAT GGG TCT TGC CCC AGG ACA GTA CAT	338
Ala Ala Phe Cys Tyr Gln Val Asn Gly Ser Cys Pro Arg Thr Val His	
15 20 25	
ACT CTG GGC ATC CAG TTG GTC ATC TAC CTG ACC TGT GCA GCA GGC ATG	386
Thr Leu Gly Ile Gln Leu Val Ile Tyr Leu Thr Cys Ala Ala Gly Met	
30 35 40 45	
CTG ATT ATC GTG CTA GGG AAT GTA TTT GTG GCA TTT GCT GTG TCC TAC	434
Leu Ile Ile Val Leu Gly Asn Val Phe Val Ala Phe Ala Val Ser Tyr	
50 55 60	
TTC AAA GCG CTT CAC ACG CCC ACC AAC TTC CTG CTG CTC TCC CTG GCC	482
Phe Lys Ala Leu His Thr Pro Thr Asn Phe Leu Leu Leu Ser Leu Ala	
65 70 75	
CTG GCT GAC ATG TTT CTG GGT CTG CTG GTG CTG CCC CTC AGC ACC ATT	530
Leu Ala Asp Met Phe Leu Gly Leu Leu Val Leu Pro Leu Ser Thr Ile	
80 85 90	
CGC TCA GTG GAG AGC TGC TGG TTC TTC GGG GAC TTC CTC TGC CGC CTG	578
Arg Ser Val Glu Ser Cys Trp Phe Phe Gly Asp Phe Leu Cys Arg Leu	
95 100 105	
CAC ACC TAC CTG GAC ACC CTC TTC TGC CTC ACC TCC ATC TTC CAT CTC	626
His Thr Tyr Leu Asp Thr Leu Phe Cys Leu Thr Ser Ile Phe His Leu	
110 115 120 125	
TGT TTC ATT TCC ATT GAC CGC CAC TGT GCC ATC TGT GAC CCC CTG CTC	674
Cys Phe Ile Ser Ile Asp Arg His Cys Ala Ile Cys Asp Pro Leu Leu	
130 135 140	
TAT CCC TCC AAG TTC ACA GTG AGG GTG GCT CTC AGG TAC ATC CTG GCA	722
Tyr Pro Ser Lys Phe Thr Val Arg Val Ala Leu Arg Tyr Ile Leu Ala	
145 150 155	
GGA TGG GGG GTG CCC GCA GCA TAC ACT TCG TTA TTC CTC TAC ACA GAT	770
Gly Trp Gly Val Pro Ala Ala Tyr Thr Ser Leu Phe Leu Tyr Thr Asp	
160 165 170	

GTG GTA GAG ACA AGG CTC AGC CAG TGG CTG GAA GAG ATG CCT TGT GTG Val Val Glu Thr Arg Leu Ser Gln Trp Leu Glu Glu Met Pro Cys Val 175 180 185	818
GGC AGT TGC CAG CTG CTG CTC AAT AAA TTT TGG GGC TGG TTA AAC TTC Gly Ser Cys Gln Leu Leu Leu Asn Lys Phe Trp Gly Trp Leu Asn Phe 190 195 200 205	866
CCT TTG TTC TTT GTC CCC TGC CTC ATT ATG ATC AGC TTG TAT GTG AAG Pro Leu Phe Phe Val Pro Cys Leu Ile Met Ile Ser Leu Tyr Val Lys 210 215 220	914
ATC TTT GTG GTT GCT ACC AGA CAG GCT CAG CAG ATT ACC ACA TTG AGC Ile Phe Val Val Ala Thr Arg Gln Ala Gln Gln Ile Thr Thr Leu Ser 225 230 235	962
AAA AGC CTG GCT GGG GCT GCC AAG CAT GAG AGA AAA GCT GCC AAG ACC Lys Ser Leu Ala Gly Ala Ala Lys His Glu Arg Lys Ala Ala Lys Thr 240 245 250	1010
CTG GGC ATT GTT GTG GGC ATA TAC CTC TTG TGC TGG CTG CCC TTC ACC Leu Gly Ile Val Val Gly Ile Tyr Leu Leu Cys Trp Leu Pro Phe Thr 255 260 265	1058
ATA GAC ACG ATG GTC GAC AGC CTC CTT CAC TTT ATC ACA CCC CCA CTG Ile Asp Thr Met Val Asp Ser Leu Leu His Phe Ile Thr Pro Pro Leu 270 275 280 285	1106
GTC TTT GAC ATC TTT ATC TGG TTT GCT TAC TTC AAC TCA GCC TGC AAC Val Phe Asp Ile Phe Ile Trp Phe Ala Tyr Phe Asn Ser Ala Cys Asn 290 295 300	1154
CCC ATC ATC TAT GTC TTT TCC TAC CAG TGG TTT CGG AAG GCA CTG AAA Pro Ile Ile Tyr Val Phe Ser Tyr Gln Trp Phe Arg Lys Ala Leu Lys 305 310 315	1202
CTC ACA CTG AGC CAG AAG GTC TTC TCA CCG CAG ACA CGC ACT GTT GAT Leu Thr Leu Ser Gln Lys Val Phe Ser Pro Gln Thr Arg Thr Val Asp 320 325 330	1250
TTG TAC CAA GAA TGATTCCTTC TACTAAATGC AGGCAAGGAG TAGGACCTCA Leu Tyr Gln Glu	1302
335	
CAGGAAAGAT AAGTGGCACT GTGACCGCGG GCTGTGTGGT GTTGAGTTTG TGGGCATGCT	1362
TCCAGGACAG CATGGGTT	1380

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Arg	Ala	Val	Phe	Ile	Gln	Gly	Ala	Glu	Glu	His	Pro	Ala	Ala	Phe	1	5	10	15
Cys	Tyr	Gln	Val	Asn	Gly	Ser	Cys	Pro	Arg	Thr	Val	His	Thr	Leu	Gly	20	25	30	
Ile	Gln	Leu	Val	Ile	Tyr	Leu	Thr	Cys	Ala	Ala	Gly	Met	Leu	Ile	Ile	35	40	45	
Val	Leu	Gly	Asn	Val	Phe	Val	Ala	Phe	Ala	Val	Ser	Tyr	Phe	Lys	Ala	50	55	60	
Leu	His	Thr	Pro	Thr	Asn	Phe	Leu	Leu	Leu	Ser	Leu	Ala	Leu	Ala	Asp	65	70	75	80
Met	Phe	Leu	Gly	Leu	Leu	Val	Leu	Pro	Leu	Ser	Thr	Ile	Arg	Ser	Val	85	90	95	
Glu	Ser	Cys	Trp	Phe	Phe	Gly	Asp	Phe	Leu	Cys	Arg	Leu	His	Thr	Tyr	100	105	110	
Leu	Asp	Thr	Leu	Phe	Cys	Leu	Thr	Ser	Ile	Phe	His	Leu	Cys	Phe	Ile	115	120	125	
Ser	Ile	Asp	Arg	His	Cys	Ala	Ile	Cys	Asp	Pro	Leu	Leu	Tyr	Pro	Ser	130	135	140	
Lys	Phe	Thr	Val	Arg	Val	Ala	Leu	Arg	Tyr	Ile	Leu	Ala	Gly	Trp	Gly	145	150	155	160
Val	Pro	Ala	Ala	Tyr	Thr	Ser	Leu	Phe	Leu	Tyr	Thr	Asp	Val	Val	Glu	165	170	175	
Thr	Arg	Leu	Ser	Gln	Trp	Leu	Glu	Glu	Met	Pro	Cys	Val	Gly	Ser	Cys	180	185	190	
Gln	Leu	Leu	Leu	Asn	Lys	Phe	Trp	Gly	Trp	Leu	Asn	Phe	Pro	Leu	Phe	195	200	205	
Phe	Val	Pro	Cys	Leu	Ile	Met	Ile	Ser	Leu	Tyr	Val	Lys	Ile	Phe	Val	210	215	220	
Val	Ala	Thr	Arg	Gln	Ala	Gln	Gln	Ile	Thr	Thr	Leu	Ser	Lys	Ser	Leu	225	230	235	240
Ala	Gly	Ala	Ala	Lys	His	Glu	Arg	Lys	Ala	Ala	Lys	Thr	Leu	Gly	Ile	245	250	255	
Val	Val	Gly	Ile	Tyr	Leu	Leu	Cys	Trp	Leu	Pro	Phe	Thr	Ile	Asp	Thr	260	265	270	
Met	Val	Asp	Ser	Leu	Leu	His	Phe	Ile	Thr	Pro	Pro	Leu	Val	Phe	Asp	275	280	285	
Ile	Phe	Ile	Trp	Phe	Ala	Tyr	Phe	Asn	Ser	Ala	Cys	Asn	Pro	Ile	Ile				

10021 54233550

290 295 300  
 Tyr Val Phe Ser Tyr Gln Trp Phe Arg Lys Ala Leu Lys Leu Thr Leu  
 305 310 315 320  
 Ser Gln Lys Val Phe Ser Pro Gln Thr Arg Thr Val Asp Leu Tyr Gln  
 325 330 335  
 Glu

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGGAATTCCT UATGAGAGCT GTCTTCATC

29

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGAAGCTTC GTCATTCTTG GTACAAATCA AC

32

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

T0027-5128860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGGATCCCT CCATGAGAGC TGTCTTCATC

30

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGGGATCCCG CTCATTCTTG GTACAAATC

29

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTCCAAGCTT GCCACCATGA GAGCTGTCTT CATC

34

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTAGCTCGAG TCAAGCGTAG TCTGGGACGT CGTATGGGTA GCATTCTTGG TACAAATCAA

60

C

61

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala 1	Arg	Leu	Leu	Val 5	Leu	Ala	Ser	Pro	Pro 10	Ala	Ser	Leu	Leu	Pro 15	Pro
Ala	Ser	Glu	Gly 20	Ser	Ala	Pro	Leu	Ser 25	Gln	Gln	Trp	Thr	Ala 30	Gly	Met
Gly	Leu	Leu	Val 35	Ala	Leu	Ile	Val 40	Leu	Leu	Ile	Val	Val 45	Gly	Asn	Val
Leu	Val 50	Ile	Val	Ala	Ile	Ala 55	Lys	Thr	Pro	Arg	Leu 60	Gln	Thr	Leu	Thr
Asn 65	Leu	Phe	Ile	Met	Ser 70	Leu	Ala	Ser	Ala	Asp 75	Leu	Val	Met	Gly	Leu 80
Leu	Val	Val	Pro	Phe 85	Gly	Ala	Thr	Ile	Val 90	Val	Trp	Gly	Arg	Trp 95	Glu
Tyr	Gly	Ser	Phe 100	Phe	Cys	Glu	Leu	Trp 105	Thr	Ser	Val	Asp	Val 110	Leu	Cys
Val	Thr 115	Ala	Ser	Ile	Glu	Thr	Leu 120	Cys	Val	Ile	Ala	Leu 125	Asp	Arg	Tyr
Leu	Ala 130	Ile	Thr	Ser	Pro	Phe 135	Arg	Tyr	Gln	Ser	Leu 140	Leu	Thr	Arg	Ala
Arg 145	Ala	Arg	Ala	Leu	Val 150	Cys	Thr	Val	Trp	Ala 155	Ile	Ser	Ala	Leu	Val 160
Ser	Phe	Leu	Pro	Ile 165	Leu	Met	His	Trp	Trp 170	Arg	Ala	Glu	Ser	Asp 175	Glu
Ala	Arg	Arg	Cys 180	Tyr	Asn	Asp	Pro	Lys 185	Cys	Cys	Asp	Phe	Val 190	Thr	Asn
Arg	Ala	Tyr 195	Ala	Ile	Ala	Ser	Ser 200	Val	Val	Ser	Phe	Tyr 205	Val	Pro	Leu
Cys	Ile 210	Met	Ala	Phe	Val	Tyr 215	Leu	Arg	Val	Phe	Arg 220	Glu	Ala	Gln	Lys

Gln Val Lys Lys Ile Asp Ser Cys Glu Arg Arg Phe Leu Gly Gly Pro  
 225 230 235 240

Ala Arg Pro Pro Ser Pro Glu Pro Ser Pro Ser Pro Gly Pro Pro Arg  
 245 250 255

Pro Ala Asp Ser Leu Ala Asn Gly Arg Ser Ser Lys Arg Arg Pro Ser  
 260 265 270

Arg Leu Val Ala Leu Arg Glu Gln Lys Ala Leu Lys Thr Leu Gly Ile  
 275 280 285

Ile Met Gly Val Phe Thr Leu Cys Trp Leu Pro Phe Phe Leu Ala Asn  
 290 295 300

Val Val Lys Ala Phe His Arg Asp Leu Val Pro Asp Arg Leu Phe Val  
 305 310 315 320

Phe Phe Asn Trp Leu Gly Tyr Ala Asn Ser Ala Phe Asn Pro Ile Ile  
 325 330 335

Tyr Cys Arg Ser Pro Asp Phe Arg Lys Ala Phe Gln Arg Leu Leu Cys  
 340 345 350

Cys Ala Arg Arg Ala Ala Cys Arg Arg Arg Ala Ala His  
 355 360 365

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asp Asp Asp Leu Glu Arg Gln Asn Trp Ser Arg Pro Phe Asn Gly Ser  
 1 5 10 15

Asp Gly Lys Ala Asp Arg Pro His Tyr Asn Tyr Tyr Ala Thr Leu Leu  
 20 25 30

Thr Leu Leu Ile Ala Val Ile Val Phe Gly Asn Val Leu Val Cys Met  
 35 40 45

Ala Val Ser Arg Glu Lys Ala Leu Gln Thr Thr Thr Asn Tyr Leu Ile  
 50 55 60

Val Ser Leu Ala Val Ala Asp Leu Leu Val Ala Thr Leu Val Met Pro  
 65 70 75 80

FOOCT" 54/99660



Trp Val Val Tyr Leu Glu Val Val Gly Glu Trp Lys Phe Ser Arg Ile  
85 90 95

His Cys Asp Ile Phe Val Thr Leu Asp Val Met Met Cys Thr Ala Ser  
100 105 110

Ile Leu Asn Leu Cys Ala Ile Ser Ile Asp Arg Tyr Thr Ala Val Ala  
115 120 125

Met Pro Met Leu Tyr Asn Thr Arg Tyr Ser Ser Lys Arg Arg Val Thr  
130 135 140

Val Met Ile Ser Ile Val Trp Val Leu Ser Phe Thr Ile Ser Cys Pro  
145 150 155 160

Leu Leu Phe Gly Leu Asn Asn Ala Asp Gln Asn Glu Cys Ile Ile Ala  
165 170 175

Asn Pro Ala Phe Val Val Tyr Ser Ser Ile Val Ser Phe Tyr Val Pro  
180 185 190

Phe Ile Val Thr Leu Leu Val Tyr Ile Lys Ile Tyr Ile Val Leu Arg  
195 200 205

Arg Arg Arg Lys Arg Val Asn Thr Lys Arg Ser Ser Arg Ala Phe Arg  
210 215 220

Ala His Leu Arg Ala Pro Leu Lys Glu Ala Ala Arg Arg Glu Lys Asn  
225 230 235 240

Gly His Ala Lys Asp His Pro Lys Ile Ala Lys Ile Phe Glu Ile Gln  
245 250 255

Thr Met Pro Asn Gly Lys Thr Arg Thr Ser Leu Lys Thr Met Ser Arg  
260 265 270

Arg Lys Leu Ser Gln Gln Lys Glu Lys Lys Ala Thr Gln Met Leu Ala  
275 280 285

Ile Val Leu Gly Val Phe Ile Ile Cys Trp Leu Pro Phe Phe Ile Thr  
290 295 300

His Ile Leu Asn Ile His Cys Asp Cys Asn Ile Pro Pro Val Leu Tyr  
305 310 315 320

Ser Ala Phe Thr Trp Leu Gly Tyr Val Asn Ser Ala Val Asn Pro Ile  
325 330 335

Ile Tyr Thr Thr Phe Asn Ile Glu Phe Arg Lys Ala Phe Leu Lys Ile  
340 345 350

Leu

Protein 222660